

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 7, 2001, 23:28:44 ; Search time 69.91 seconds
(without alignments)
8025.979 Million cell updates/sec

Title: US-09-349-954A-5
Perfect score: 993
Sequence: 1 ccatgagccctctctcgc.....gaagaaaaa 993

Scoring table: IDENTITY_NTC
Gapop 10.0, Gapext 1.0

Searched: 470478 seqs, 282525781 residues

Total number of hits satisfying chosen parameters: 940956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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2: /cgnl_7/ptodata/1/pna/US06_NEW_COMB.seq:*
3: /cgnl_7/ptodata/1/pna/US07_NEW_COMB.seq:*
4: /cgnl_7/ptodata/1/pna/US08_NEW_COMB.seq:*
5: /cgnl_7/ptodata/1/pna/US09_NEW_COMB.seq:*
6: /cgnl_7/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	409.8	41.3	449	US-09-737-223-13904	Sequence 13904, A
2	255.4	25.7	257	US-09-442-385-872	Sequence 872, App
3	238.8	24.0	478	US-09-737-223-35423	Sequence 35423, A
4	92.2	9.3	516	US-09-812-133-1	Sequence 1, Appl1
5	79.2	8.0	425	US-09-442-385-898	Sequence 898, App
6	66.2	6.7	1941	US-09-783-514-2135	Sequence 2135, App
7	64	6.4	475	US-09-737-223-1813	Sequence 1813, App
8	47.6	4.8	445	US-09-737-223-35222	Sequence 35222, A
9	45.6	4.5	1118	US-09-739-449-1169	Sequence 1169, App
10	44.2	4.5	565	US-09-624-658-85	Sequence 85, Appl
11	44	4.4	456	US-09-640-2114-195	Sequence 195, App
12	42.4	4.3	3152	PCT-US01-04098A-210	Sequence 210, App
13	42.4	4.3	3236	PCT-US01-04098A-2178	Sequence 2178, App
14	42.2	4.2	4403765	US-09-103-840A-2	Sequence 2, Appl1
15	41.8	4.2	3046	US-09-783-514-1823	Sequence 1823, App
16	41.8	4.2	12279	US-09-783-514-1915	Sequence 1915, App
17	41.6	4.2	12279	US-09-654-835A-99	Sequence 99, Appl1
18	40.8	4.1	4403765	US-09-103-840A-2	Sequence 2, Appl1
19	40.8	4.1	4411529	US-09-103-840A-1	Sequence 1, Appl1
20	40.2	4.0	288	US-09-807-521-546	Sequence 546, App
21	40.2	4.0	1384	PCT-US01-01335-628	Sequence 628, App
22	40.2	4.0	1384	PCT-US01-01335-628	Sequence 628, App
23	40.2	4.0	1386	PCT-US01-01335-629	Sequence 629, App
24	40	4.0	1602	US-09-833-790-417	Sequence 417, App
25	40	4.0	101880	US-60-248-505-650	Sequence 650, App
26	39.2	3.9	540	US-09-724-866A-9259	Sequence 9259, App
27	39.2	3.9	12133	US-60-248-823-30	Sequence 30, Appl

28	39	3.9	1492	US-60-248-505-1935	Sequence 1935, App
29	39	3.9	1829	US-09-828-366-15	Sequence 15, Appl
30	38.8	3.9	925	US-09-739-449-1170	Sequence 1170, App
31	38.8	3.9	154746	PCT-US01-11372-8	Sequence 8, Appl1
32	38.8	3.9	134746	US-09-827-688-8	Sequence 8, Appl1
33	38.6	3.9	2700	US-09-826-508-25	Sequence 25, Appl
34	38.6	3.9	2826	US-09-818-879-46	Sequence 46, Appl
35	38.4	3.9	871	US-09-739-449-1174	Sequence 1174, App
36	38.4	3.9	1280	US-09-670-314-4	Sequence 4, Appl1
37	38.4	3.9	1938	PCT-US01-01339-8557	Sequence 8557, App
38	38.4	3.9	1938	PCT-US01-01339-8558	Sequence 8558, App
39	38.4	3.9	1938	PCT-US01-01329-3085	Sequence 3085, App
40	38.4	3.9	1938	PCT-US01-01329-3086	Sequence 3086, App
41	38.4	3.9	2205	US-09-833-129-14	Sequence 14, Appl
42	37.8	3.8	539	US-09-270-849B-3425	Sequence 3425, App
43	37.6	3.8	519	US-09-724-866A-12915	Sequence 12915, A
44	37.6	3.8	1116	US-09-739-449-589	Sequence 589, App
45	37.6	3.8	1286	PCT-US01-04098A-2066	Sequence 2066, App

ALIGNMENTS

RESULT 1
US-09-737-223-13904
Sequence 13904, Application US/09737223
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FILE REFERENCE: 20411-756
CURRENT FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: 09/737,223
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 13904
LENGTH: 449
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc:feature
LOCATION: (1)-(449)
OTHER INFORMATION: n = A,T,C or G
US-09-737-223-13904

Query Match 41.3%; Score 409.8; DB 5; Length 449;
Best Local Similarity 99.5%; Pred. No. 9.3e-85;
Matches 411; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	492	cgagctccctccgcttgcgaagggcggttcagagctcaagccagacacgtgagtcg	551
DB	37	cgagctccctccgcttgcgaagggcggttcagagctcaagccagacacgtgagtcg	96
QY	552	cggaagctgcgaagtgacacatgctttcagactcagcaggggtgactgctcagag	611
DB	97	cgaagctgcgaagtgacacatgctttcagactcagcaggggtgactgctcagag	156
QY	612	ctatataccatgtggggaacaaaggagctgtttaaaacacagcccaagacc	671
DB	157	ctataccatgtggggaacaaaggagctgtttaaaacacagcccaagacc	216
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DB	217	tcagccagcagagagctgtcctcagagcctgcctcagagggctcttcgcatcc	276
QY	732	ttgtctccctgagggcattcacaacagagagagttggaagagagactggaagc	791
DB	277	ttgtctccctgagggcattcacaacagagagagttggaagagagactggaagc	336
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OM nucleic - nucleic search, using sw model

Run on: June 7, 2001, 23:31:10 / Search time 1856.6 Seconds
(without alignments)
7379.021 Million cell updates/sec

Title: US-09-349-954A-5
Perfect score: 993
Sequence: 1 ccatgagccctctcgcgc.....gaagaaaaaaaaaaaaa 993

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1316883 seqs, 689823319 residues
Total number of hits satisfying chosen parameters: 26337766

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 59: /cgml_7/ptodata/1/pna/US6027_COMB.seq:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, evaluated at the total score distribution.

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 7, 2001, 23:27:30 ; Search time 64.32 Seconds
(without alignments)
2695.592 Million cell updates/sec

Title: US-09-349-954A-5

Perfect score: 993
Sequence: 1 catgagccctctgtctgcgc.....gaaggaaaaaaaaaaaaa 993

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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4: /cgnl_7/ptodata/1/ina/6B.COMB.seq:*
5: /cgnl_7/ptodata/1/ina/PCTUS.COMB.seq:*
6: /cgnl_7/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	567.4	57.1	570	1 US-08-469-427A-10	Sequence 10, Appl
2	567.4	57.1	570	2 US-08-609-443B-10	Sequence 10, Appl
3	567.4	57.1	570	2 US-08-569-063C-10	Sequence 10, Appl
4	469	47.2	565	1 US-08-469-427A-4	Sequence 4, Appl
5	469	47.2	565	2 US-08-609-443B-4	Sequence 4, Appl
6	469	47.2	565	2 US-08-569-063C-4	Sequence 4, Appl
7	442	44.5	591	1 US-08-469-427A-6	Sequence 6, Appl
8	442	44.5	591	2 US-08-609-443B-6	Sequence 6, Appl
9	442	44.5	591	2 US-08-569-063C-6	Sequence 6, Appl
10	412.2	41.5	886	1 US-08-469-427A-1	Sequence 1, Appl
11	412.2	41.5	886	2 US-08-609-443B-1	Sequence 1, Appl
12	412.2	41.5	886	2 US-08-569-063C-1	Sequence 1, Appl
13	408.8	41.2	624	2 US-08-609-443B-14	Sequence 14, Appl
14	408.8	41.2	624	2 US-08-569-063C-14	Sequence 14, Appl
15	338	34.0	624	2 US-08-609-443B-12	Sequence 12, Appl
16	338	34.0	624	2 US-08-569-063C-12	Sequence 12, Appl
17	319.6	32.2	405	1 US-08-469-427A-8	Sequence 8, Appl
18	319.6	32.2	405	2 US-08-609-443B-8	Sequence 8, Appl
19	319.6	32.2	405	2 US-08-569-063C-8	Sequence 8, Appl
20	97.2	9.8	605	3 US-08-718-904-2	Sequence 2, Appl
21	97.2	9.8	605	5 PCT-US95-10973A-26	Sequence 26, Appl
22	96	9.7	599	5 PCT-US95-10973A-87	Sequence 87, Appl
23	96	9.7	599	5 PCT-US95-10973A-89	Sequence 89, Appl
24	96	9.7	990	6 5332671-11	Patent No. 5332671
25	96	9.7	990	3 US-08-567-200A-1	Sequence 1, Appl
26	96	9.7	990	3 US-08-691-794-1	Sequence 1, Appl
27	96	9.7	1299	5 PCT-US95-10973A-58	Sequence 58, Appl

28	96	9.7	1809	5 PCT-US95-10973A-79	Sequence 79, Appl
29	94.4	9.5	498	6 5194596-20	Patent No. 5194596
30	94.4	9.5	498	6 5219739-21	Patent No. 5219739
31	93	9.4	1269	5 PCT-US95-10973A-32	Sequence 32, Appl
32	93	9.4	1369	5 PCT-US95-10973A-33	Sequence 33, Appl
33	92.2	9.3	467	5 PCT-US95-10973A-86	Sequence 86, Appl
34	92.2	9.3	467	5 PCT-US95-10973A-88	Sequence 88, Appl
35	92.2	9.3	473	3 US-08-718-904-1	Sequence 1, Appl
36	92.2	9.3	516	3 PCT-US95-10973A-25	Sequence 25, Appl
37	92.2	9.3	516	3 US-08-784-551C-1	Sequence 1, Appl
38	92.2	9.3	648	4 US-08-586-039B-48	Sequence 48, Appl
39	92.2	9.3	774	4 US-08-765-340-1	Sequence 1, Appl
40	92.2	9.3	1167	5 PCT-US95-10973A-57	Sequence 57, Appl
41	92.2	9.3	1195	6 5240848-6	Patent No. 5240848
42	92.2	9.3	1212	5 PCT-US95-10973A-31	Sequence 31, Appl
43	92.2	9.3	1557	5 PCT-US95-10973A-78	Sequence 78, Appl
44	90.8	9.1	677	3 US-08-718-904-3	Sequence 3, Appl
45	90.8	9.1	677	5 PCT-US95-10973A-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-08-469-427A-10
Sequence 10, Application US/08469427A
Patent No. 5607918
GENERAL INFORMATION:
APPLICANT: Eriksso, Ulf
APPLICANT: Olofsson, Birgitta
APPLICANT: Allitalo, Karl
APPLICANT: Pajusola, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
TITLE OF INVENTION: DNA CODING THEREFOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Evenson, McKewen, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,427A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 41979cp2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 570 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: human fibrosarcoma
US-08-469-427A-10